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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seq2-seq4.res made by mruhl on Wed 29 Jan 103 17:52:07-PST.


Query sequence being compared:US-09-531-266-2 (1-360)
Number of sequences searched:              2
Number of scores above cutoff:             2

        Results of the initial comparison of US-09-531-266-2 (1-360) with:
            File : US09531266.pep


    100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                                *
N     -
C     -
E     -
S     0-------------------------------------------------------------------------
        |       |       |       |       |       |       |       |       |
SCORE 0    40      80     120     160     200     240     280     320     360
STDEV
```
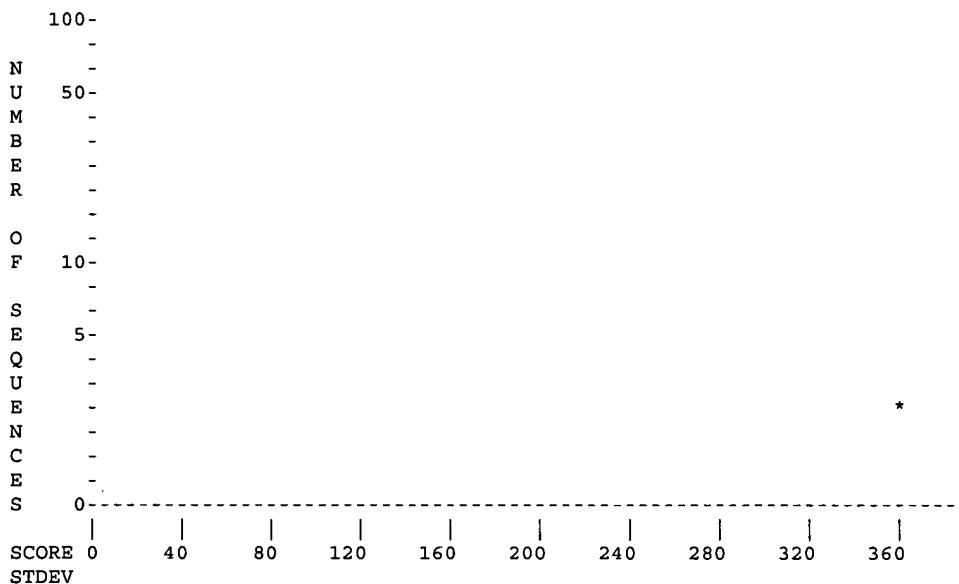
                            PARAMETERS

Similarity matrix   PAM-150   K-tuple   2
Threshold level of sim.   16%
Mismatch penalty   1   Joining penalty   20
Gap penalty   5.00   Window size   360
Gap size penalty   0.05
Cutoff score   1
Randomization group   0

                        SEARCH STATISTICS

Scores: Mean   Median   Standard Deviation
                        360   361   0.00

Times: CPU   Total Elapsed
                    00:00:00.00   00:00:00.00

Number of residues: 720
Number of sequences searched: 2
Number of scores above cutoff: 2

The scores below are sorted by initial score.
Significance is calculated based on initial score.

2 100% identical sequences to the query sequence were found:

```
                                                   Init. Opt.
Sequence Name      Description                  Length Score Score  Sig. Frame
-------------------------------------------------------------------------------
   1. US-09-531-266-4 Sequence 4, Application US   360   360   360   0.00   0


1. US-09-531-266-2 (1-360)
   US-09-531-266-4 Sequence 4, Application US/09531266

Initial Score     =    360  Optimized Score  =    360  Significance = 0.00
Residue Identity  =   100%  Matches          =    360  Mismatches   =    0
Gaps              =      0  Conservative Substitutions           =    0

   X        10        20        30        40        50        60        70
   MSHIDDLAQLGTSTWLDDLSRERITSGNLSQVIEEKSVVGVTTNPAIFAAAMSKGDSYDAQIAELKAAGASV
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   MSHIDDLAQLGTSTWLDDLSRERITSGNLSQVIEEKSVVGVTTNPAIFAAAMSKGDSYDAQIAELKAAGASV
   X        10        20        30        40        50        60        70


           80        90       100       110       120       130       140
   DQAVYAMSIDDVRNACDLFTGIFESSNGYDGRVSIEVDPRISADRDATLAQAKELWAKVDRPNVMIKIPATP
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   DQAVYAMSIDDVRNACDLFTGIFESSNGYDGRVSIEVDPRISADRDATLAQAKELWAKVDRPNVMIKIPATP
           80        90       100       110       120       130       140


      150       160       170       180       190       200       210
   GSLPAITDALAEGISVNVTLIFSVARYREVIAAFIEGIKQAAANGHDVSKIHSVASFFVSRVDVEIDKRLEA
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   GSLPAITDALAEGISVNVTLIFSVARYREVIAAFIEGIKQAAANGHDVSKIHSVASFFVSRVDVEIDKRLEA
      150       160       170       180       190       200       210


   220       230       240       250       260       270       280
   IGSDEALALRGKAGVANAQRAYAVYKELFDAAELPEGANTQRPLWASTGVKNPAYAATLYVSELAGPNTVNT
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   IGSDEALALRGKAGVANAQRAYAVYKELFDAAELPEGANTQRPLWASTGVKNPAYAATLYVSELAGPNTVNT
   220       230       240       250       260       270       280


290       300       310       320       330       340       350         X
   MPEGTIDAVLEQGNLHGDTLSNSAAEADAVFSQLEALGVDLADVFQVLETEGVDKFVASWSELLESMEARLK
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   MPEGTIDAVLEQGNLHGDTLSNSAAEADAVFSQLEALGVDLADVFQVLETEGVDKFVASWSELLESMEARLK
290       300       310       320       330       340       350       360
```